ABSTRACT

A control method, apparatus, and system to actively assure the quality of a biological sample through genetic or nucleic acid sequence screening. The genetic information from the biological sample is sequenced and associated with patient

5   information, such as patient name or other patient identifier. The genetic sequence is then compared with other entries in a sequence database to determine the closest matches within the database, and further compared with a confidence threshold. A report may then be generated indicating whether the closest matches within the confidence threshold match the patient information. The quality assurance integrity of the biological sample

10   can be determined when the patient information of the biological sample matches previous samples from the same patient.